

Application No. 09/857,315
Amdt. dated September 8, 2006
Reply to Office Action of June 8, 2006

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Having regard thereto, it is submitted that claims 19, 22 and 24 to 28 are no longer open to provisional rejection under the judicially created doctrine of obviousness-type double patenting as being unpatentable over claims 19, 20, 22 and 24 to 28 of co-pending Application no. 10/699,683 and hence the rejection should be withdrawn.

The Examiner rejected claims 19, 22, 24, 25, 27 and 28 under 35 U.S.C. 102(e) as being anticipated by Murdin et al U.S. Patent nos. 6,693,087 or 6,686,339. Reconsideration is requested.

The Examiner states that:

"Murdin et al., for example 6,696,087 (the Examiner means 6,693,087) discloses a nucleic acid molecule encoding an outer membrane protein (MOMP) of a strain of *Chlamydia* (abstract)."

The abstract of Murdin et al 6,693,087 states:

"An isolated and purified nucleic acid molecule encoding a POMP91A protein of a strain of *Chlamydia*..." (emphasis added)

The abstract does not mention MOMP but rather a quite different protein of *Chlamydia*. Similarly, the "Abstract" of Murdin et al 6,686,339 states:

"....method of nucleic acid,.... immunization of a host,....employing a vector, containing a nucleotide sequence encoding an inclusion membrane protein C of a strain of *Chlamydia*...." (emphasis added)

This inclusion membrane protein C to which Murdin et al 6,686,339 relates is a further, different protein from MOMP.

Enclosed for the Examiner's consideration is a sequence comparison for the amino acid sequences from the MOMP, POMP91A and InC proteins of *Chlamydia pneumoniae*. The sequence comparison was prepared using the CLUSTAL W (1.83) multiple sequence alignment at the default settings. For the

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convenience of the Examiner, enclosed are the annotated sequences used to prepare the alignments. It can be seen that there is no similarity among the three sequences.

The Examiner does not indicate in the Office Action wherein is the Murdin et al reference there is disclosed a vector comprising a nucleic acid molecule encoding MOMP. It is submitted that the only vectors disclosed are molecules containing the nucleic acid molecule encoding POMP91 (US 6,693,087) or encoding inclusion membrane protein C (US 6,686,339).

Accordingly, it is submitted that applicant's pending claims are not anticipated by either Murdin et al reference and hence the rejection of claims 19, 22, 24, 25, 27 and 28 under 35 U.S.C.102(e) as being anticipated by Murdin et al (6,693,087 or 6,686,339), should be withdrawn.

The Examiner rejected claim 26 under 35 U.S.C. 103(a) over Murdin et al. (6,693,087 or 6,686,339) as applied to claims 19, 22, 24, 25, 27 and 28 and further in view of Brunham (WO 98/02546). Claim 26 is dependent, indirectly, on claim 19 and recites that the plasmid vector is pcDNA3/MOMP.

The Murdin et al references have been discussed above. As set forth in that discussion, the Murdin et al reference does not disclose a vector comprising a nucleic acid molecule encoding MOMP.

Brunham describes the vector pcDNA3/MOMP, there is no motivation provided by Brunham or Murdin et al to substitute this vector for the vectors described in Murdin in an attenuated bacterium environment.

Accordingly, it is submitted that claim 26 is patentable over the applied art and hence the rejection thereof under 35 U.S.C. 103(a) as being unpatentable over either Murdin et al reference in view of Brunham, should be withdrawn.

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It is believed that this application is now in condition for allowance and early and favourable consideration and allowance are respectfully solicited.

Respectfully submitted,



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! Sequence: momp
! Sequence: incC
! Sequence: pomp91a
CLUSTAL W (1.83) multiple sequence alignment

```
momp      -----  
incC      -----  
pomp91a    MEIQMRLWGFILFLSSFCQVSYLRANDVLLPLSGIHSGEDLELFTLRSSSPTKTTYSLRKDF  
  
momp      -----MKKLLKSVLVFAALSSASSLQALFVG--  
incC      -----MTSPIPFQ--  
pomp91a    IVCDFAGNSIHKPGAFLNLKGDLEFFINSTFLAALTFKNIHLGARGAGLFESNVTFKGL  
          : . . .  
  
momp      -----NPAEPSLMIDGILWEGFGGDPDPCATWCDASIMAVGYGDFVF  
incC      -----SSGDASFLAEQFQQLPSTSESQVLTQLLTMMKHTQALSETVLQQ  
pomp91a    HSLVLENNE SWGGVLTTSGDLSFINNTSVLCQNNISYGPGGALLQGRKSKALFFRDNRG  
          : . . . : . . .  
  
momp      -----DLVLKTDVNKEFQMGAKPTTDTGNSAAPS-----  
incC      -----QADRLEPTASIILOVGGAPTGGAGAPFQPG-----  
pomp91a    TILFLKNKAVNQDESHPGYGGAVSSISPGSPITFADNQEILFQENEGELGGAIYNDQGA  
          : . . . : . . .  
  
momp      -----TLTARENPAYGRHMQDAEMFTNAACMALNIWDR--  
incC      -----PADDHHHPPIPPFVPAQIETEITTIRSELQLMR--  
pomp91a    TFENNFQTTSFSSNKASFEELSIAATAISIHSGAIPYSLKTLLOKLGGATHADYVHIRDC  
          : . . . : . . .  
  
momp      -----FDVFCTLGATSGYLKGNASAFNLVGLFGDNENQKTVKAESVPMMSFDQSVVELYTDTT  
incC      -----STLQQSTKGARTGVLVVTTAILMTISLLAIIIIILAVLGFTG---VLPOVALLMQGETN  
pomp91a    HGSIVFEENSATAGGATAVNAVCDINAQGFVRFINNSALGLNGGAIYMQATGSILALHAN  
          : . . . : . . .  
  
momp      -----FAWSVGARAALWECGCATLG---  
incC      -----LIWAMVSGSIIICFIALIG---  
pomp91a    QGDIEFCGNKVRSQFHSHINSTSNFTNNAITIQGAPREFSLSANEGHRICFYDPIISATE  
          : . . . : . . .  
  
momp      -----  
incC      -----  
pomp91a    GYNSLYINHQRLLLEAGGAVIFSGARLSPEHKKENKNKTSIINQPVRLCSGVLSIEGGAIL  
  
momp      -----ASFQYAQSKPKVEELNVLNAAEF  
incC      -----TLGLILTNKNTPLPAS-----  
pomp91a    AVRSFYQEGGLLALGPGSKLTTQGNSEKDKIVITNLGFNLNLDSSDPAEIRATEKASI  
          : . . . : . . .  
  
momp      -----PINKPKGYVGKEFPLOLTAGTDAATG-----  
incC      -----EISGVPRVYGHTESFYENHEYASKFYTTSIILSAKKLVTPSRPEKDIQNLIIAESEYMG  
pomp91a  
  
momp      -----TKDASIDYHEWQASLALSYRLNMFTPYIGVKWSRASFDADTIRIA  
incC      -----  
pomp91a    YGYQGSWEFSWSFNDTKEKKTIIASWTPTGFEFLDPKRRGSFPTTLWSTFSGLNIAJNI  
  
momp      -----  
incC      -----  
pomp91a    QPKSATAIFDTTTLNPTIAGAGDVKTGAEGQLGDTMQIVSLQLNKMKSRSKCGIAVGTTI  
          : . . . : . . .
```

pomp91a	VNNNYLNNSEVIPLQHL CVFGGFVYQIMEQNPKQSSNNLLVQHAGHNVGARIPFSFNTIL
momp	VCADKYAVTVETRLIDERA AHVNAQFRF-----
incC	-----
pomp91a	SAALTQLFSSSSQONVADKSHAQILIGTVSLNKSQALSLRSSFSYTEDSQVMKHVFPYK
momp	-----
incC	-----
pomp91a	G)SRGSWRNYGWSGSVGMSYAYPKGIRYLKMTPFVDLQYTKLVQNPFVETGYDPRYFSSS
momp	-----
incC	-----
pomp91a	EMTNLSLPIGIALEMRFIGSRSSSLFLQVSTSYIKOLRRVNPQSSASLVLNHYTWDIQGVF
momp	-----
incC	-----
pomp91a	LGKEALNITLNSTIKYKIVTAYMGISSTQREGSNLSANAHAGLSLSF

"*" means that the residues or nucleotides in that column are identical in all sequences in the alignment
 "." means that conserved substitutions have been observed
 "-" means that semi-conserved substitutions are observed

6693087pomp91a seq
947 aa linear PAT 20-FEB-2004

LOCUS AAS37561
DEFINITION Sequence from patent US 6693087.
ACCESSION AAS37561
VERSION AAS37561.1 GI:42715796
DBSOURCE accession AAS37561.1
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (residues 1 to 947)
AUTHORS Murdin,A.D., Dunn,P.L. and Oomen,R.P.
TITLE Nucleic acid molecules encoding POMP91A protein of Chlamydia
JOURNAL Patent: US 6693087-A 3 17-FEB-2004;
Aventis Pasteur Limited; Toronto;
CAX;
REMARK CAMBIA Patent Lens: US 6693087
FEATURES Location/Qualifiers
source 1..947
/organism="unknown"

ORIGIN
1 mkqmrllwgfl flssfcqvsv lrandvllpl sgihsgegle lftlrssst kttyslckdf
61 ivcdfagnsi hkpgaafnl kgdlffinst plaaltfkni hlqargaglf sesnvtfkgf
121 hslvlennes wggvlttsqd lsfintsvl cqnnsyggp galllqgrks kalffrdnrg
181 tilflknkav ngdeshpgyg gavssispgs pitfadnqei lfgenegeig gaiyndggai
241 tfennfqttt ffsnkastee lsiaataisi hsgaipyslk tllqklggai hadyvhirdc
301 kgsivfeens ataggaiavn avcdinaqgp vrfinnsalg lnggaiymqa tgsilrlhan
361 qgdiefcgnk vrsqfhshin stsnftnnai tiqgaprefs lsaneghric fydpiisate
421 nyslyinhq rllleaggavi fsgarlspch kkenknktsi inqpvrllcsg visieggail
481 ayrsfyqegg llaigpgskl ttqgknsekd kivitnlgnf lenldssdpa eiratekasi
541 eisgvprvyg htesfyenhe yaskpyttsi ilsakkltva psrpekdiqn liiaeseymg
601 ygyqgsweff wspndtkekk tiiaswtptg efsldpkrrg sfipttlwst fsglniasni
661 vnnnylnnse viplqlcvf ggpvygimeq npkqssnnll vqhaghnvga ripfsntil
721 saaltqlfss ssqnvadks haqiligtvs lnkswgalsl rssfyteds qvmkhvfpyk
781 gtsrgswrny gwsqsvqmsy aypkgirylk mtpfvdlqyt klvqnpfvet gydpryfss
841 emtnlslpig ialemrfigs rslflqvst syikdlrrvn pqssaslvln hytwdiqgvp
901 lgkealniti nstikykiat aymgisstqr egslsanah aglsisf

66863391ncc seq 203 aa linear PAT 20-FEB-2004

LOCUS AAS33023
 DEFINITION Sequence from patent US 6686339.
 ACCESSION AAS33023
 VERSION AAS33023.1 GI:42707452
 DBSOURCE accession AAS33023.1
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (residues 1 to 203)
 AUTHORS Murdin,A.D., Dunn,P.L. and Oomen,R.P.
 TITLE Nucleic acid molecules encoding inclusion membrane protein C of
 Chlamydia
 JOURNAL Patent: US 6686339-A 3 03-FEB-2004;
 Aventis Pasteur Limited; Toronto;
 CAX;
 REMARK CAMBIA Patent Lens: US 6686339
 FEATURES Location/Qualifiers
 source 1..203
 /organism="unknown"

ORIGIN
 1 mtspipfqs gdsflaeqp qqlpstsesq lvtqlltmmk htgalsetvl qqqrdr1pta
 61 siilqvvgap tggagapfqp gpaddhhhpi pppvvpaqie teittirsel qlmrstlqqs
 121 tkgartgvlv vtailmtisl laiiiiiilav lgftgvlpqv allmqgetnl iwamvsgsli
 181 cfialigtlg liltknkntpl pas

stephens momp
393 aa linear BCT 02-MAY-2006

LOCUS Q46409
DEFINITION Major outer membrane protein, serovar D precursor (MOMP).
ACCESSION Q46409
VERSION Q46409 GI:6707730
DBSOURCE swissprot: locus OM1D_CHLTR, accession Q46409;
class: standard.
created: May 30, 2000.
sequence updated: Nov 1, 1996.
annotation updated: May 2, 2006.
xrefs: X62918.1, CAA44701.1, AF063195.2, AAC31436.2, AE001273.1,
AAC68276.1, H71484
xrefs (non-sequence databases): PHCI-2DPAGE:Q46409,
GenomeReviews:AE001273_GR, InterPro:IPR000604, Pfam:PF01308,
PRINTS:PR01334

KEYWORDS Complete proteome; Ion transport; Membrane; Outer membrane; Porin;
Signal; Transmembrane; Transport.

SOURCE Chlamydia trachomatis
ORGANISM Chlamydia trachomatis
Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.

REFERENCE 1 (residues 1 to 393)
AUTHORS Sayada, C., Denamur, E. and Elion, J.
TITLE Complete sequence of the major outer membrane protein-encoding gene
of Chlamydia trachomatis serovar Da
JOURNAL Gene 120 (1), 129-130 (1992)
PUBMED 1398119
REMARK NUCLEOTIDE SEQUENCE [GENOMIC DNA].
STRAIN=D/B-120

REFERENCE 2 (residues 1 to 393)
AUTHORS Stothard, P.R., Boguslawski, G. and Jones, R.B.
TITLE Phylogenetic analysis of the Chlamydia trachomatis major outer
membrane protein and examination of potential pathogenic
determinants
JOURNAL Infect. Immun. 66 (8), 3618-3625 (1998)
PUBMED 9673241
REMARK NUCLEOTIDE SEQUENCE [GENOMIC DNA].
STRAIN=D/IU-71960

REFERENCE 3 (residues 1 to 393)
AUTHORS Stephens, R.S., Kalman, S., Lammel, C., Fan, J., Marathe, R.,
Aravind, L., Mitchell, W., Olinger, L., Tatusov, R.L., Zhao, Q.,
Koonin, E.V. and Davis, R.W.
TITLE Genome sequence of an obligate intracellular pathogen of humans:
Chlamydia trachomatis
JOURNAL Science 282 (5389), 754-759 (1998)
PUBMED 9784136
REMARK NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
STRAIN=D/UW-3/Cx

COMMENT On Sep 27, 2005 this sequence version replaced gi:7442973.
[FUNCTION] Structural rigidity of the outer membrane of elementary
bodies and porin forming, permitting diffusion of solutes through
the intracellular reticulate body membrane.
[SUBUNIT] Disulfide bond interactions within and between MOMP
molecules and other components form high molecular-weight
oligomers.
[SUBCELLULAR LOCATION] Bacterial cell outer membrane; multi-pass
membrane protein.
[SIMILARITY] Belongs to the chlamydial OMP family.

FEATURES
source Location/Qualifiers
1..393
/organism="Chlamydia trachomatis"
/db_xref="taxon:813"
gene 1..393
/gene="ompA"
/locus_tag="CT_681"


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                                stephens momp
Protein    /note="synonym: omp1"
           /gene="ompA"
           /locus_tag="CT_681"
           /product="Major outer membrane protein, serovar D
           /precursor"
Region     /gene="ompA"
           /locus_tag="CT_681"
           /region_name="Signal"
           /inference="non-experimental evidence, no additional
           details recorded"
           /note="By similarity."
Region     /gene="ompA"
           /locus_tag="CT_681"
           /region_name="Mature chain"
           /experiment="experimental evidence, no additional details
           recorded"
           /note="Major outer membrane protein, serovar D."
           /FTId=PRO_0000020147."
ORIGIN
1 mkkllksvly faalssassl qalpvgnpae pslmidgilw egfggdpcdp catwcdaism
61 rvgyygdvfv drvlktdvnk efqmgakptt dtgnsaapst ltarenpayg rhmqdaemft
121 naacmalniw drfdvfcrlg atsgylkgnv asfnlvglfg dnengktvka esvpnmfsdq
181 svveltdttt fawsvgaraa lwecgcatlg asfqyagskp kveelnvln aaftinkpk
241 gyvgkefpld ltagtdaatg tkdasidyhe wqasialsyf lnmftpyigv kwsrasfdad
301 tiriaqpkas taifdtttln ptiagagdvk tgaegqlgdt mqivslqlnk mksrkscgia
361 vgttividak yavtvetrli deraahvnaq frf

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